Amendments to the claims:

Claim 1 (Previously Presented): A method of modifying an antibiotic-producing strain of *Streptomyces coelicolor* to increase antibiotic production in said strain, the method comprising functionally deleting in said strain the *scbA* gene by introducing a deletion, stop codon or frameshift into the coding sequence of said gene, wherein before said introduction said scbA gene encodes a polypeptide having the amino acid sequence of SEQ ID NO: 17.

Claims 2-8 (Cancelled)

Claim 9 (Previously Presented): A modified strain of *Streptomyces coelicolor*, the modified strain having a functional deletion of the *scbA* gene, said functional deletion being effected by introducing a deletion, stop codon or frameshift into the coding sequence of said gene, whereby production of at least one antibiotic in said modified strain is increased compared to a wild-type strain of *Streptomyces coelicolor*, wherein before said introduction said scbA gene encodes a polypeptide having the amino acid sequence of SEQ ID NO: 17.

Claim 10 (Cancelled)

Claim 11 (Previously Presented): The method of claim 1, wherein the strain is *S. coelicolor* A3(2).

Claim 12 (Cancelled)

Claim 13 (Previously Presented): The strain of claim 9, which is a modified strain of *S. coelicolor* A3(2).

Claim 14 (Cancelled)

Claim 15 (Currently Amended): A method for identifying

Streptomyces species in which antibiotic production is increased by the functional deletion of the *scbA* gene of *S. coelicolor* or a homolog thereof, said scbA gene having a nucleotide sequence which:

(a) is the complement of nucleotides 2142-1199 of SEQ ID NO: 19; and/or

(b) encodes a polypeptide having the amino acid sequence of SEQ ID NO: 17;

and said homologue having a nucleotide sequence which has at least 90% sequence homology to the complement of nucleotides 2142-1199 of SEQ ID NO: 19;

the method comprising functionally deleting the *scbA* gene of *S. coelicolor* or said homolog thereof in an antibiotic-producing strain of a *Streptomyces* species by introducing a deletion, stop codon or frameshift into the coding sequence of said gene, the effect of said deletion on increasing said antibiotic production in said antibiotic-producing strain being unknown, said species being other than *S. virginiae* and *S. griseus*, culturing said strain under conditions suitable for the production of antibiotic, and determining whether antibiotic production in said strain is increased.

Claims 16-22 (Cancelled)

Claim 23 (Previously Presented): The method of claim 15, wherein said sequence identity is at least 95%.